EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	379368	tolerance or tolerize or toleragenic	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L2	335	mHag or (minor adj histocompatibility adj antigen)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L3	254065	transplant or transplantation or transplanted or transplanting or graft or grafted or grafting	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L4	177929	reject or rejection	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L5	100	L1 and L2 and L3 and L4	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L6	2371	HA-1 or ha1 or (ha adj "1")	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L7	379368	tolerance or tolerize or toleragenic	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L8	36942	((514/2) or (514/8) or (514/12) or (530/350) or (530/328) or (530/327)).CCLS.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	OFF	2006/08/29 14:20
L9	247	L8 and L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L10	105	L9 and L7	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:21
L11	2371	HA-1 or ha1 or (ha adj "1")	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:21

L12	12816	GvHD or GvH or (graft adj versus adj (host or leukemia)) or GvL	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:21
L13	6757711	treat or treatment or prevent or prevention or eliminate or elimination or therapy or therapeutic	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L14	11	L11 and L1 and L2 and L12 and L3 and L4 and L13	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:20
L15	8250	goulmy.in. or hunt.in. or englhard.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:22
L16	8536	goulmy.in. or hunt.in. or engelhard.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:22
L17	311	l16 and (l7 or l6 or l2)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:23
L18	14	l16 and l7 and (l6 or l2)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/29 14:23

SCORE Search Results Details for Application 10623176 and Search Result us-10-623-176a-2.rag.

This page gives you Search Results detail for the Application 10623176 and Search Result us-10-623-176a-2.rag.

start

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 18, 2006, 00:39:56 ; Search time 191 Seconds
                                             (without alignments)
                                             21.544 Million cell updates/sec

Title: US-10-623-176A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
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Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 442222

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

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Result            Query
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     4     37     82.2      9     2    AAW99197             Aaw99197 Minor his
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    30     26     57.8      9     8    ADT49074             Adt49074 Human BFA
    31     26     57.8      9     8    ADU99636             Adu99636 BFA5 tumo
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    34     25     55.6      9     4    AAG79144             Aag79144 Amino ter
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    40     24     53.3      7     2    AAW33386             Aaw33386 Altered I
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ALIGNMENTS

RESULT 1
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ID   AAW99196 standard; peptide; 9 AA.
XX
AC   AAW99196;
XX
DT   20-MAY-1999   (first entry)

SCORE Search Results Details for Application 10623176 and Search Result us-10-623-176a-2.rai.

This page gives you Search Results detail for the Application 10623176 and Search Result us-10-623-176a-2.rai.

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                         GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:          August 18, 2006, 00:49:01 ; Search time 49 Seconds
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Title:           US-10-623-176A-2
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         and is derived by analysis of the total score distribution.

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Result              Query
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   3    37    82.2   9   2   US-09-269-250E-18        Sequence 18, Appl
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   7    30    66.7   9   2   US-09-489-760-4          Sequence 4, Appli
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   9    28    62.2   9   2   US-09-776-232-52         Sequence 52, Appl
  10    28    62.2   9   2   US-09-380-534-52         Sequence 52, Appl
  11    26    57.8   6   2   US-10-166-225A-163       Sequence 163, App
  12    26    57.8   6   2   US-10-166-225A-164       Sequence 164, App
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  17    25    55.6   7   2   US-09-025-819-5          Sequence 5, Appli
  18    25    55.6   7   2   US-09-808-126-5          Sequence 5, Appli
  19    25    55.6   7   2   US-09-803-951-5          Sequence 5, Appli
  20    25    55.6   9   2   US-08-582-333A-3         Sequence 3, Appli
  21    25    55.6   9   2   US-09-305-923A-7         Sequence 7, Appli
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  26    24    53.3   9   3   US-09-641-528B-48631     Sequence 48631, A
  27    23    51.1   6   2   US-09-217-609A-8         Sequence 8, Appli
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  35    22    48.9   7   1   US-08-428-823-9          Sequence 9, Appli
  36    22    48.9   7   2   US-08-556-419-14         Sequence 14, Appl
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ALIGNMENTS

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US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21

SCORE Search Results Details for Application 10623176 and Search Result us-10-623-176a 2.rapbm.

This page gives you Search Results detail for the Application 10623176 and Search Result us-10-6: 2.rapbm.

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                        GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:          August 18, 2006, 01:00:36 ; Search time 179 Seconds
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                                             23.290 Million cell updates/sec

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     Pred. No. is the number of results predicted by chance to have a
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3	45	100.0	9	5	US-10-861-335-1	Sequence 1, Appli
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5	45	100.0	9	6	US-11-010-748A-11	Sequence 11, Appl
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8	37	82.2	9	4	US-10-623-176-10	Sequence 10, Appl
9	37	82.2	9	4	US-10-623-176-47	Sequence 47, Appl
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28	28	62.2	9	4	US-10-777-053-95	Sequence 95, Appl
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ALIGNMENTS

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US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18

SCORE Search Results Details for Application 10623176 and Search Result us-10-623-176a-2.rapbn.

This page gives you Search Results detail for the Application 10623176 and Search Result us-10-6: 176a-2.rapbn.

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                    GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:          August 18, 2006, 01:01:12 ; Search time 32 Seconds
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Title:           US-10-623-176A-2
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Sequence:        1 VLHDDLLEA 9

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Post-processing: Minimum Match 0%
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     and is derived by analysis of the total score distribution.

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4	23	51.1	9	6	US-10-537-642-611	Sequence 611, App
5	22	48.9	8	7	US-11-122-986-753	Sequence 753, App
6	22	48.9	9	6	US-10-781-659-25	Sequence 25, Appl
7	21	46.7	9	7	US-11-140-487A-1758	Sequence 1758, Ap
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15	20	44.4	7	6	US-10-479-225A-20	Sequence 20, Appl
16	20	44.4	7	7	US-11-398-130-8	Sequence 8, Appli
17	19	42.2	7	7	US-11-122-986-362	Sequence 362, App
18	19	42.2	7	7	US-11-263-230-1202	Sequence 1202, Ap
19	19	42.2	7	7	US-11-263-230-1486	Sequence 1486, Ap
20	19	42.2	7	7	US-11-263-230-1487	Sequence 1487, Ap
21	19	42.2	7	7	US-11-398-130-16	Sequence 16, Appl
22	19	42.2	9	6	US-10-537-642-323	Sequence 323, App
23	19	42.2	9	6	US-10-570-010-25	Sequence 25, Appl
24	19	42.2	9	7	US-11-140-487A-1828	Sequence 1828, Ap
25	18	40.0	7	7	US-11-263-230-362	Sequence 362, App
26	18	40.0	7	7	US-11-263-230-651	Sequence 651, App
27	18	40.0	7	7	US-11-263-230-790	Sequence 790, App
28	18	40.0	7	7	US-11-263-230-934	Sequence 934, App
29	18	40.0	7	7	US-11-263-230-1067	Sequence 1067, Ap
30	18	40.0	7	7	US-11-263-230-1346	Sequence 1346, Ap
31	18	40.0	8	7	US-11-223-610-23	Sequence 23, Appl
32	18	40.0	8	7	US-11-234-731-622	Sequence 622, App
33	18	40.0	9	6	US-10-781-659-60	Sequence 60, Appl
34	18	40.0	9	6	US-10-537-642-471	Sequence 471, App
35	18	40.0	9	7	US-11-140-487A-1073	Sequence 1073, Ap
36	18	40.0	9	7	US-11-140-487A-1227	Sequence 1227, Ap
37	18	40.0	9	7	US-11-122-986-817	Sequence 817, App
38	18	40.0	9	7	US-11-240-651-10	Sequence 10, Appl
39	18	40.0	9	7	US-11-011-026-24	Sequence 24, Appl
40	18	40.0	9	7	US-11-313-152-155	Sequence 155, App
41	18	40.0	9	7	US-11-313-152-417	Sequence 417, App
42	17	37.8	6	7	US-11-178-155-13	Sequence 13, Appl
43	17	37.8	6	7	US-11-287-157A-163	Sequence 163, App
44	17	37.8	7	1	US-09-906-481E-7	Sequence 7, Appli
45	17	37.8	7	7	US-11-023-959A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-11-313-152-52
; Sequence 52, Application US/11313152
; Publication No. US20060153858A1
; GENERAL INFORMATION:
; APPLICANT: Kundig, Thomas M.
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE
; FILE REFERENCE: MANNK.001CP2C1

SCORE Search Results Details

This page gives you Search Results detail for the Application 10623176 and Search Result us-10-6:

start

```
                          GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Bioccceleration Ltd.


OM protein - protein search, using sw model

Run on:          August 18, 2006, 00:44:01 ; Search time 38 Seconds
                                             (without alignments)
                                             22.788 Million cell updates/sec

Title:           US-10-623-176A-2
Perfect score:   45
Sequence:        1 VLHDDLLEA 9

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	40.0	7	2	I46868	alpha-myosin heavy
2	17	37.8	9	2	S55696	phosphoenolpyruvat
3	16	35.6	7	2	PQ0663	membrane protein -
4	16	35.6	7	2	S68004	hucolin, 75K chain
5	16	35.6	8	2	PC4131	hypothetical prote
6	15	33.3	6	2	S78764	ribosomal protein
7	15	33.3	7	2	A59489	protein kinase C i
8	14	31.1	7	2	S20446	elastase - Pseudom

```
 9    14   31.1    8   2   XGHUEU              urine glycopeptide
10    14   31.1    9   2   A12872              transaldolase (EC
11    14   31.1    9   2   S10920              venom protein HR-3
12    14   31.1    9   2   A60427              macrophage cytotox
13    13   28.9    8   2   A61328              trypsin (EC 3.4.21
14    13   28.9    9   2   PH0942              T-cell receptor be
15    12   26.7    4   2   I40697              biotin A - Citroba
16    12   26.7    5   2   PT0679              T-cell receptor be
17    12   26.7    5   2   PT0601              T-cell receptor be
18    12   26.7    6   2   B35640              cerebellar degener
19    12   26.7    6   2   PT0533              T-cell receptor be
20    12   26.7    7   2   A34026              acetylcholinestera
21    12   26.7    7   2   B39040              calsequestrin, fas
22    12   26.7    7   2   PT0628              T-cell receptor be
23    12   26.7    7   2   PT0722              T-cell receptor be
24    12   26.7    7   2   PT0576              T-cell receptor be
25    12   26.7    8   2   PT0368              Ig gamma chain C r
26    12   26.7    8   2   PN0043              phosphatidylethano
27    12   26.7    8   2   PT0557              T-cell receptor be
28    12   26.7    9   2   A60108              exotoxin A - Strep
29    12   26.7    9   2   PW0002              chlorophyll a/b-bi
30    12   26.7    9   2   S65913              pyrimidine synthes
31    12   26.7    9   2   PH0108              late G1-69 protein
32    12   26.7    9   2   PT0562              T-cell receptor be
33    12   26.7    9   2   B30572              T-cell receptor be
34    11   24.4    5   2   C41225              copper resistance
35    11   24.4    5   2   T10954              hypothetical prote
36    11   24.4    6   2   T11779              phosphoglycerate t
37    11   24.4    7   2   S25266              pilE protein - Esc
38    11   24.4    7   2   PT0246              Ig heavy chain CRD
39    11   24.4    8   2   S22428              chitin-binding pro
40    11   24.4    8   2   B33099              158K exoantigen -
41    11   24.4    8   2   S69165              ferredoxin a2 - Ja
42    11   24.4    9   2   S66419              tetrameric protein
43    11   24.4    9   2   PT0272              Ig heavy chain CRD
44    11   24.4    9   2   A11497              transaldolase (EC
45    11   24.4    9   2   B39504              octamer-binding pr
```

ALIGNMENTS

RESULT 1
I46868
alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricu
A;Reference number: I46868; MUID:84221901; PMID:6328491
A;Accession: I46868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7
A;Cross-references: UNIPROT:Q28742; UNIPARC:UPI0000087938; GB:K01698; NID:g165538; PID

   Query Match   40.0%;   Score 18; DB 2; Length 7;
   Best Local Similarity 50.0%;   Pred. No. 2.8e+05;
   Matches   2; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

SCORE Search Results Details for Application 10623176 and Search Result us-10-623-176a-2.rup.

This page gives you Search Results detail for the Application 10623176 and Search Result us-10-623-176a-2.rup.

start

```
                    GenCore version 5.1.9
           Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          August 18, 2006, 00:40:41 ; Search time 295 Seconds
                                            (without alignments)
                                            28.221 Million cell updates/sec

Title:           US-10-623-176A-2
Perfect score:   45
Sequence:        1 VLHDDLLEA 9

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:     2195

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_7.2:*
                 1:  uniprot_sprot:*
                 2:  uniprot_trembl:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	42.2	9	2	Q7R8X5_PLAYO	Q7r8x5 plasmodium
2	19	42.2	9	2	Q47556_ECOLI	Q47556 escherichia
3	18	40.0	7	2	Q28742_RABIT	Q28742 oryctolagus
4	17	37.8	9	2	Q7M3S5_9TRYP	Q7m3s5 trypanosoma

5	16	35.6	7	2	O99182_9SMEG	O99182	gnatholebia
6	16	35.6	8	2	Q7Z6G0_HUMAN	Q7z6g0	homo sapien
7	16	35.6	8	2	Q2L8A3_COFCA	Q2l8a3	coffea cane
8	16	35.6	8	2	Q2L8A4_9GENT	Q2l8a4	coffea cong
9	16	35.6	9	1	FAR8_MACRS	P83281	macrobrachi
10	16	35.6	9	2	Q70SM2_HUMAN	Q70sm2	homo sapien
11	16	35.6	9	2	Q2Q2A8_CAEEL	Q2q2a8	caenorhabdi
12	16	35.6	9	2	Q4X981_PLACH	Q4x981	plasmodium
13	16	35.6	9	2	Q8LPT5_MAIZE	Q8lpt5	zea mays (m
14	16	35.6	9	2	P82568_STRPY	P82568	streptococc
15	16	35.6	9	2	Q2WDC8_FICHY	Q2wdc8	ficedula hy
16	16	35.6	9	2	Q2WDC9_FICPA	Q2wdc9	ficedula pa
17	16	35.6	9	2	Q2WDD7_FICAL	Q2wdd7	ficedula al
18	15	33.3	8	2	Q15900_HUMAN	Q15900	homo sapien
19	15	33.3	8	2	Q4XT27_PLACH	Q4xt27	plasmodium
20	15	33.3	9	2	Q9XJN0_9VIRU	Q9xjn0	bacteriopha
21	14	31.1	6	1	CWP29_ARATH	P80849	arabidopsis
22	14	31.1	6	1	TRPI_PSEPU	P36414	pseudomonas
23	14	31.1	8	1	GLUR_HUMAN	P02729	homo sapien
24	14	31.1	8	2	Q9BFA7_MACPR	Q9bfa7	macroscelid
25	14	31.1	8	2	P72279_RHOGO	P72279	rhodococcus
26	14	31.1	8	2	Q93SR0_STAEP	Q93sr0	staphylococ
27	14	31.1	8	2	Q3S8H3_9HIV1	Q3s8h3	human immun
28	14	31.1	9	1	TAL1_PICJA	P17440	pichia jadi
29	14	31.1	9	2	Q7M4R5_HUMAN	Q7m4r5	homo sapien
30	14	31.1	9	2	Q7M471_VESOR	Q7m471	vespa orien
31	14	31.1	9	2	Q9FSZ2_CICAR	Q9fsz2	cicer ariet
32	14	31.1	9	2	Q8CG39_RAT	Q8cg39	rattus norv
33	14	31.1	9	2	Q9QZA8_MOUSE	Q9qza8	mus musculu
34	14	31.1	9	2	Q6Q7G0_RANRI	Q6q7g0	rana ridibu
35	14	31.1	9	2	Q85710_9RETR	Q85710	rous sarcom
36	14	31.1	9	2	Q8UTD7_9HIV1	Q8utd7	human immun
37	13	28.9	7	2	Q66205_9CORO	Q66205	transmissib
38	13	28.9	8	2	Q9HDS4_ASPFL	Q9hds4	aspergillus
39	13	28.9	8	2	Q15889_HUMAN	Q15889	homo sapien
40	13	28.9	8	2	Q7M390_BALAC	Q7m390	balaenopter
41	13	28.9	8	2	Q37854_BPR17	Q37854	bacteriopha
42	13	28.9	8	2	Q6JC68_SOYBN	Q6jc68	glycine max
43	13	28.9	8	2	Q7XB03_MAIZE	Q7xb03	zea mays (m
44	13	28.9	8	2	Q51594_9ZZZZ	Q51594	plasmid col
45	13	28.9	9	2	Q56SS9_SAMCA	Q56ss9	sambucus ca

ALIGNMENTS

RESULT 1
Q7R8X5_PLAYO
ID   Q7R8X5_PLAYO   PRELIMINARY;   PRT;   9 AA.
AC   Q7R8X5;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Hypothetical protein.
GN   ORFNames=PY07095;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=17XNL;